

WEST Search History

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DATE: Wednesday, August 11, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L4	L2 and cinnamomensis	34
<input type="checkbox"/>	L3	monensi\$ same (polyketide adj2 (synthase or synthetase))	133
<input type="checkbox"/>	L2	monensi\$ and (polyketide adj2 (synthase or synthetase))	169
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L1	monensi\$ and (polyketide adj2 (synthase or synthetase))	64

END OF SEARCH HISTORY

09/980217
STN Search Summary

=> d his

FILE 'REGISTRY' ENTERED AT 12:19:23 ON 11 AUG 2004
L1 1 S 17090-79-8/RN
FILE 'CAPLUS' ENTERED AT 12:19:55 ON 11 AUG 2004
L2 2407 S L1
L3 7 S L2 AND (POLYKETIDE (2W) (SYNTHASE OR SYNTHETASE))
L4 79 S L1 AND CINNAMONENSIS
L5 11 S L4 AND (GENE OR ENZYME OR NUCLEOTIDE)
L6 5 S L5 NOT L3

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 17090-79-8 REGISTRY
CN Monensin (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN 1,6-Dioxaspiro[4.5]decane, monensin deriv.
CN 1,6-Dioxaspiro[4.5]decane-7-butyric acid, 2-[5-ethyltetrahydro-5-[tetrahydro-3-methyl-5-[tetrahydro-6-hydroxy-6-(hydroxymethyl)-3,5-dimethyl-2H-pyran-2-yl]-2-furyl]-2-furyl]-9-hydroxy-.beta.-methoxy-.alpha.,.gamma.,2,8-tetramethyl- (8CI)

OTHER NAMES:

CN A 3823A
CN Elancoban
CN Monelan
CN Monensic acid
CN Monensin A
CN Stereoisomer of 2-[2-ethyloctahydro-3'-methyl-5'-[tetrahydro-6-hydroxy-6-(hydroxymethyl)-3,5-dimethyl-2H-pyran-2-yl][2,2'-bifuran]-5-yl]-9-hydroxy-.beta.-methoxy-.alpha.,.gamma.,2,8-tetramethyl-1,6-dioxaspiro[4.5]decane-7-butanoic acid
DR 1392-52-5
MF C36 H62 O11

L3 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:826990 CAPLUS
TI Intermediates released from a polyether-producing polyketide synthase provide insight into the mechanism of oxidative cyclization
AU Hughes-Thomas, Zoe A.; Stark, B. W.; Boehm, Ines U.; Staunton, James; Leadlay, Peter F.
SO Angewandte Chemie, International Edition (2003), 42(37), 4475-4478

L3 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:775709 CAPLUS
TI Analysis of the biosynthetic gene cluster for the polyether antibiotic monensin in Streptomyces cinnamomensis and evidence for the role of monB and monC genes in oxidative cyclization
AU Oliynyk, Markiyana; Stark, Christian B. W.; Bhatt, Apoorva; Jones, Michelle A.; Hughes-Thomas, Zoe A.; Wilkinson, Christopher; Oliynyk, Zoryana; Demydchuk, Yuliya; Staunton, James; Leadlay, Peter F.
SO Molecular Microbiology (2003), 49(5), 1179-1190

L3 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2002:17941 CAPLUS
 TI Engineering of complex polyketide biosynthesis - insights from sequencing
 of the monensin biosynthetic gene cluster
 AU Leadlay, P. F.; Staunton, J.; Oliynyk, M.; Bisang, C.; Cortes, J.; Frost,
 E.; Hughes-Thomas, Z. A.; Jones, M. A.; Kendrew, S. G.; Lester, J. B.;
 Long, P. F.; McArthur, H. A. I.; McCormick, E. L.; Oliynyk, Z.; Stark, C.
 B. W.; Wilkinson, C. J.
 SO Journal of Industrial Microbiology & Biotechnology (2001), 27(6), 360-367

L3 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:693525 CAPLUS
 TI A type I polyketide synthase for monensin biosynthesis
 and the corresponding gene cluster of Streptomyces cinnamomensis and the
 engineering of novel polyketide synthases
 IN Leadlay, Peter Francis; Staunton, James; Oliynyk, Marko
 PATENT NO. KIND DATE APPLICATION NO. DATE

 PI WO 2001068867 A1 20010920 WO 2000-GB2072 20000530
 EP 1183369 A1 20020306 EP 2000-931459 20000530
 PRAI GB 1999-12563 A 19990528
 WO 2000-GB2072 W 20000530

L3 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2000:15378 CAPLUS
 TI Functional domains of polyketide synthetases and their
 use in the generation of novel synthetases and novel macrolide antibiotics
 IN Leadlay, Peter Francis; Staunton, James; Cortes, Jesus; McArthur, Hamish
 Alastair Irvine
 PATENT NO. KIND DATE APPLICATION NO. DATE

 PI WO 2000000618 A2 20000106 WO 1999-GB2044 19990629
 WO 2000000618 A3 20000427
 AU 9945247 A1 20000117 AU 1999-45247 19990629
 AU 763230 B2 20030717
 BR 9911712 A 20010320 BR 1999-11712 19990629
 EP 1090123 A2 20010411 EP 1999-928128 19990629
 TR 200003770 T2 20010420 TR 2000-200003770 19990629
 TR 200003771 T2 20011022 TR 2000-200003771 19990629
 JP 2002519032 T2 20020702 JP 2000-557371 19990629
 NZ 509600 A 20040326 NZ 1999-509600 19990629
 PRAI GB 1998-14006 A 19980629
 WO 1999-GB2044 W 19990629

L3 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1998:65985 CAPLUS
 TI Polyketides and their synthesis in Streptomyces strains transformed with
 hybrid type I polyketide synthases
 IN Leadlay, Peter Francis; Staunton, James; Cortes, Jesus
 PATENT NO. KIND DATE APPLICATION NO. DATE

 PI WO 9801546 A2 19980115 WO 1997-GB1819 19970704
 WO 9801546 A3 19980409
 CA 2259420 AA 19980115 CA 1997-2259420 19970704
 CA 2259463 AA 19980115 CA 1997-2259463 19970704
 AU 9734514 A1 19980202 AU 1997-34514 19970704
 AU 731654 B2 20010405

EP 910633	A2	19990428	EP 1997-930631	19970704
CN 1229438	A	19990922	CN 1997-197649	19970704
JP 2000511063	T2	20000829	JP 1998-504933	19970704
WO 9854308	A2	19981203	WO 1998-GB1559	19980528
WO 9854308	A3	19990408		
AU 9876661	A1	19981230	AU 1998-76661	19980528
EP 983348	A2	20000308	EP 1998-924463	19980528
KR 2000023579	A	20000425	KR 1999-700024	19990105
US 2002004487	A1	20020110	US 2001-896357	20010629
US 6437151	B2	20020820		
US 2003104585	A1	20030605	US 2002-307595	20021202
PRAI GB 1996-14189	A	19960705		
US 1996-24188P	P	19960819		
GB 1997-10962	A	19970528		
WO 1997-GB1819	W	19970704		
WO 1998-GB1559	W	19980528		
US 1999-214454	A3	19990916		
US 1999-424751	A1	19991129		

L3 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1987:170050 CAPLUS
 TI Homology between *Streptomyces* genes coding for synthesis of different polyketides used to clone antibiotic biosynthetic genes
 AU Malpartida, F.; Hallam, S. E.; Kieser, H. M.; Motamedi, H.; Hutchinson, C. R.; Butler, M. J.; Sugden, D. A.; Warren, M.; McKillop, C.; et al.
 SO Nature (London, United Kingdom) (1987), 325(6107), 818-21

L6 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2001:183742 CAPLUS
 TI MeaA, a putative coenzyme B12-dependent mutase, provides methylmalonyl coenzyme A for monensin biosynthesis in *Streptomyces cinnamonensis*
 AU Zhang, Weiwen; Reynolds, Kevin A.
 SO Journal of Bacteriology (2001), 183(6), 2071-2080

L6 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2000:291460 CAPLUS
 TI Molecular analysis and heterologous expression of the gene encoding methylmalonyl-coenzyme A mutase from rifamycin SV-producing strain *Amycolatopsis mediterranei* U32
 AU Zhang, Weiwen; Yang, Ling; Jiang, Weihong; Zhao, Guoping; Yang, Yinliu; Chiao, Juishen
 SO Applied Biochemistry and Biotechnology (1999), 82(3), 209-225

L6 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1999:713971 CAPLUS
 TI Role of crotonyl coenzyme A reductase in determining the ratio of polyketides monensin A and B produced by *Streptomyces cinnamonensis*
 AU Liu, Haibin; Reynolds, Kevin A.
 SO Journal of Bacteriology (1999), 181(21), 6806-6813

L6 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1999:194858 CAPLUS
 TI Overproduction of 2-ketoisovalerate and monensin production by regulatory mutants of *Streptomyces cinnamonensis* resistant to 2-ketobutyrate and amino acids
 AU Pospisil, S.; Kopecky, J.; Prikrylova, V.; Spizek, J.
 SO FEMS Microbiology Letters (1999), 172(2), 197-204

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 19:13:20 ; Search time 44373 Seconds
(without alignments)
11835.746 Million cell updates/sec

Title: US-09-980-217-2 COPY 12448_24564 = monAIV coding region
Perfect score: 12117
Sequence: 1 atgtcgtgagtgctgaagagtc.....acaaagaactgggtgtgtga 12117

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	12117	100.0	30000	6	AX250262 <i>wo 01/68867</i>	AX250262 Sequence
2	12117	100.0	103450	1	AF440781 <i>GenBank 2001</i>	AF440781 Streptomy
3	4440.6	36.6	30000	6	AX250263	AX250263 Sequence
4	3934	32.5	132544	1	AF521085 <i>GB 2002</i>	AF521085 Streptomy
5	3580.8	29.6	30000	6	AX250261	AX250261 Sequence
6	3485.6	28.8	113193	1	AF357202 <i>GB 2001</i>	AF357202 Streptomy
7	3485.6	28.8	113193	6	AX703543 <i>wo 02/97082</i>	AX703543 Sequence <i>S. nodosus</i>
8	3228.6	26.6	65140	6	AX211705 <i>wo 01/59162</i>	AX211705 Sequence <i>S. noursei</i>
9	3228.6	26.6	123580	1	AF263912 <i>GB ↑</i>	AF263912 Streptomy
10	3228.6	26.6	125401	6	AX211739	AX211739 Sequence
c 11	3009.8	24.8	132544	1	AF521085	AF521085 Streptomy
c 12	2976.2	24.6	104326	1	AB070940	AB070940 Streptomy
13	2976.2	24.6	281450	1	AP005032	AP005032 Streptomy
14	2803.2	23.1	20394	1	SNA132222	AJ132222 Streptomy
15	2803.2	23.1	20394	6	AX067996	AX067996 Sequence
c 16	2803.2	23.1	84985	1	SNA278573	AJ278573 Streptomy
c 17	2786.4	23.0	138203	1	AY310323	AY310323 Streptomy
c 18	2727.4	22.5	290850	1	SCO939127	AL939127 Streptomy
19	2684.6	22.2	78210	1	AB070949	AB070949 Streptomy
c 20	2679.2	22.1	300425	1	AP005022	AP005022 Streptomy
21	2670.8	22.0	104326	1	AB070940	AB070940 Streptomy
c 22	2670.8	22.0	320150	1	AP005033	AP005033 Streptomy
23	2666.8	22.0	27541	6	AX211706	AX211706 Sequence
24	2536.4	20.9	75236	6	AX600586	AX600586 Sequence
c 25	2506.4	20.7	30000	6	AX250263	AX250263 Sequence
c 26	2506.4	20.7	103450	1	AF440781	AF440781 Streptomy
27	2473.6	20.4	69644	1	AY179507	AY179507 Streptomy
28	2454.2	20.3	50000	6	AX089417	AX089417 Sequence
29	2454.2	20.3	50000	6	AX089420	AX089420 Sequence
30	2454.2	20.3	80161	1	AY007564	AY007564 Saccharop
31	2454.2	20.3	80161	6	AR165018	AR165018 Sequence
32	2454.2	20.3	80161	6	AR281866	AR281866 Sequence
33	2454.2	20.3	80161	6	BD137649	BD137649 Biosynthe

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:41:04 ; Search time 3880 Seconds
(without alignments)
13266.860 Million cell updates/sec

Title: US-09-980-217-2_COPY_12448_24564
Perfect score: 12117
Sequence: 1 atgtcgagtgtgctgaagagtc.....acaaagaactgggtgtgtga 12117
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB			
	1	12117	100.0	103599	4	ABX04971	Abx04971	S. cinnam
	2	3485.6	28.8	113193	7	AAD54645	Aad54645	Streptomy
	3	3228.6	26.6	65140	4	AAD17184	Aad17184	Streptomy
	4	3228.6	26.6	125401	4	AAD17186	Aad17186	Streptomy
	5	2803.2	23.1	20394	4	AAF24892	Aaf24892	Pimaricin
	6	2666.8	22.0	27541	4	AAD17185	Aad17185	Streptomy
	7	2536.4	20.9	75236	7	ABV75557	Abv75557	Saccharop
c	8	2506.4	20.7	103599	4	ABX04971	Abx04971	S. cinnam
	9	2454.2	20.3	50000	4	AAF88313	Aaf88313	S. spinos
	10	2454.2	20.3	50000	4	AAF88316	Aaf88316	S. spinos
	11	2454.2	20.3	80161	2	AAZ21501	Aaz21501	DNA fragm
	12	2454	20.3	16767	4	AAF88339	Aaf88339	S. spinos
	13	2386.8	19.7	15872	3	AAZ87283	Aaz87283	S. venezu
	14	2375.6	19.6	53789	2	AAV21187	Aav21187	Amycolato
	15	2367.6	19.5	15872	2	AAT68715	Aat68715	Streptomy
	16	2110.4	17.4	67251	9	ADC26995	Adc26995	Sorangium

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:38:04 ; Search time 830 Seconds
(without alignments)
8101.614 Million cell updates/sec

Title: US-09-980-217-2_COPY_12448_24564
Perfect score: 12117
Sequence: 1 atgtcgagtgtctgaagagtc.....acaaagaactgggtgtgtga 12117
Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0
Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2454.2	20.3	80161	3	US-09-036-987A-1	Sequence 1, Appli
2	2454.2	20.3	80161	3	US-09-370-700-1	Sequence 1, Appli
3	2454.2	20.3	80161	4	US-09-603-207-1	Sequence 1, Appli
4	2386.8	19.7	15872	3	US-09-105-537-1	Sequence 1, Appli
5	2386.8	19.7	15872	4	US-09-091-609-1	Sequence 1, Appli
6	2386.8	19.7	15872	4	US-09-091-609-3	Sequence 3, Appli
7	2030.2	16.8	44377	2	US-08-804-227C-7	Sequence 7, Appli
8	2030.2	16.8	44377	2	US-08-804-198-1	Sequence 1, Appli
9	1999	16.5	50937	3	US-09-428-517-1	Sequence 1, Appli
c 10	1984.6	16.4	77536	4	US-09-410-551B-1	Sequence 1, Appli
11	1967.2	16.2	43280	2	US-08-804-227C-1	Sequence 1, Appli
12	1965.8	16.2	33529	3	US-09-144-085-3	Sequence 3, Appli
c 13	1954	16.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	1943	16.0	38506	3	US-09-320-878-19	Sequence 19, Appl
15	1943	16.0	38506	4	US-09-141-908-1	Sequence 1, Appli
16	1943	16.0	38506	4	US-09-657-440-19	Sequence 19, Appl
17	1939.4	16.0	11220	3	US-09-105-537-32	Sequence 32, Appl
18	1939.4	16.0	36778	3	US-09-105-537-5	Sequence 5, Appli
c 19	1933.8	16.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
20	1854	15.3	20235	1	US-07-642-734C-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 20:43:23 ; Search time 4567 Seconds
(without alignments)
12154.381 Million cell updates/sec

Title: US-09-980-217-2_COPY_12448_24564

Perfect score: 12117

Sequence: 1 atgtcgagtgtgaagagtc.....acaaagaactgggtgtgtga 12117

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c	1	2976.2	24.6	125746	15	US-10-156-761-15102	Sequence 15102, A
	2	2976.2	24.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
	3	2963.2	24.5	11910	15	US-10-156-761-2879	Sequence 2879, Ap
	4	2679.2	22.1	23238	15	US-10-156-761-415	Sequence 415, App
	5	2679.2	22.1	100000	15	US-10-156-761-15103	Sequence 15103, A
c	6	2679.2	22.1	9025608	15	US-10-156-761-1	Sequence 1, Appli
	7	2670.8	22.0	125746	15	US-10-156-761-15102	Sequence 15102, A